# Supplementary Data

Supplementary Table S1. Primers Employed in Amplification and Sequencing (*env* and *tax*) of Proviral DNA of Human T Lymphotropic Virus Type 2 in Patients Coinfected with HIV-1 from Southern and Southeastern Brazil

| *Molecular assay* | *Primer* | *Sequence 5′–3′ and product size* | *Position*[a] |
|---|---|---|---|
| PCR *env*[b] | E5 Forward | AGC CAA GTG TCC CTT CGA CTA (21 bp) | 5603–5623 |
| | E2 Reverse | CTG CAG AAG CTA GCA GGT CTA (21 bp) | 6641–6661 |
| n-PCR *env*[b,c] | E3 Forward | TTC TCT AAG TGC GGC TCC TC (20 bp) | 5627–5646 |
| | E2 Reverse | CTG CAG AAG CTA GCA GGT CTA (21 bp) | 6641–6661 |
| Sequencing *env*[b] | GP21F1 Forward | CTG CAA CAA CTC CAT TAT CCT (21 bp) | 6031–6051 |
| PCR *tax*[d] | Px101 Forward | GGC AAT CTC CTA AAA TAG TCT (21 bp) | 7155–7175 |
| | Px106 Reverse | GGG CCG TGG TTT CAG TTC CTA (21 bp) | 8306–8326 |
| n-PCR *tax*[c,d] | Px103 Forward | TTA CAA TCC TGT CTC CTC TCA (21 bp) | 7192–7212 |
| | Px106 Reverse | GGG CCG TGG TTT CAG TTC CTA (21 bp) | 8306–8326 |
| Sequencing *tax*[d] | Px105 Forward | GCT YTC CCC ACC CAT GAC ATG (21 bp) | 7683–7703 |
| | LS1 Forward | GAA TAC ACC AAC ATC CCT GTC (21 bp) | 8140–8160 |
| | Px102 Reverse | TGT GTG TAG GAA CAT TTT GTA (21 bp) | 7795–7815 |

[a]Primer nucleotide position is provided as aligned with Mo (HTLV-2-infected cell line; GenBank AN M10060).
[b]Adapted from Egan *et al*. (1999)[23] and Shindo *et al*. (2002).[24]
[c]Primers employed in n-PCR and sequencing.
[d]Adapted from Eiraku *et al*. (1996).[13]
Y, Highlighted degenerate nucleotide.
bp, base pairs; PCR, polymerase chain reaction; n-, nested.